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OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/942,935

DATE: 12/13/2001
 TIME: 13:47:30

Input Set : A:\032301.216.seq.ST25.txt
 Output Set: N:\CRF3\12132001\I942935.raw

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3 <110> APPLICANT: Degussa AG
 5 <120> TITLE OF INVENTION: Nucleotide Sequences Coding for the sigM Gene
 7 <130> FILE REFERENCE: 000449 BT
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/942,935
 C--> 9 <141> CURRENT FILING DATE: 2001-12-13
 9 <160> NUMBER OF SEQ ID NOS: 4
 11 <170> SOFTWARE: PatentIn version 3.1
 13 <210> SEQ ID NO: 1
 14 <211> LENGTH: 1211
 15 <212> TYPE: DNA
 16 <213> ORGANISM: Corynebacterium glutamicum
 18 <220> FEATURE:
 19 <221> NAME/KEY: CDS
 20 <222> LOCATION: (236)..(907)
 21 <223> OTHER INFORMATION:
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 25 gacaccaatc cacagatgca gatcgctgaa gtacaacttg ttggttggtta aattacgcgt 60
 27 ttgtgattga ccccccattaa ggtgcgcccg ccctcagttt cactaactga aggcgggcgt 120
 29 ttttaattta tatatagctt cagctcacag gtattttcca gaaagaagag ccctcaaagt 180
 31 atgtagcacc tcagcgacac ctcccacttg agtgggcgcc gagaagtatc tctca atg 238
 32 Met
 33 1
 35 gaa aat ctg ccc ata cta agc cgc ata agg gat acg ggg tgt gtc cct 286
 36 Glu Asn Leu Pro Ile Leu Ser Arg Ile Arg Asp Thr Gly Cys Val Pro
 37 5 10 15
 39 caa cct gcg ggg gat ctt atg aca gta ctg cct aaa aac cat gac cta 334
 40 Gln Pro Ala Gly Asp Leu Met Thr Val Leu Pro Lys Asn His Asp Leu
 41 20 25 30
 43 agc gat acc caa ctc gtc aaa cag ttt ata tct ggc gac tcc agg gca 382
 44 Ser Asp Thr Gln Leu Val Lys Gln Phe Ile Ser Gly Asp Ser Arg Ala
 45 35 40 45
 47 ttt tcc acc atc att cac cgc cac gaa cga cat atg atg cag gca gcc 430
 48 Phe Ser Thr Ile Ile His Arg His Glu Arg His Met Met Gln Ala Ala
 49 50 55 60 65
 51 aga aaa tac ggg cgg aaa cca gaa gac gcc caa gac att ctc caa gaa 478
 52 Arg Lys Tyr Gly Arg Lys Pro Glu Asp Ala Gln Asp Ile Leu Gln Glu
 53 70 75 80
 55 gct ctc ttt cgc gcc agc cga aac atg cac ctt tat aga gca gaa gca 526
 56 Ala Leu Phe Arg Ala Ser Arg Asn Met His Leu Tyr Arg Ala Glu Ala
 57 85 90 95
 59 gct ctc ggc acg tgg ctc cac aaa ctt gtc ctg aat agc ggc ttc gat 574
 60 Ala Leu Gly Thr Trp Leu His Lys Leu Val Leu Asn Ser Gly Phe Asp
 61 100 105 110
 63 tgg gct acc cac cgc tcc caa gta gaa ttc ccc atc ctt aac gaa cca 622
 64 Trp Ala Thr His Arg Ser Gln Val Glu Phe Pro Ile Leu Asn Glu Pro
 65 115 120 125
 67 aca atc gat tta gaa aaa gat cct cgc cta gcc acc gac ccc ttg ggc 670

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68 Thr Ile Asp Leu Glu Lys Asp Pro Arg Leu Ala Thr Asp Pro Leu Gly
69 130          135          140          145
71 tac ctc gat gtc gcc atg aca att cga tcc gcc atc gac caa tta cac      718
72 Tyr Leu Asp Val Ala Met Thr Ile Arg Ser Ala Ile Asp Gln Leu His
73          150          155          160
75 ccc gat caa cgc atc gcc tta ata ctt gtc gac ctc ggc ggc tac acc      766
76 Pro Asp Gln Arg Ile Ala Leu Ile Leu Val Asp Leu Gly Gly Tyr Thr
77          165          170          175
79 gta gaa gat gtg gcc gaa atc gaa gga atc aaa gta ggt acc gtt aaa      814
80 Val Glu Asp Val Ala Glu Ile Glu Gly Ile Lys Val Gly Thr Val Lys
81          180          185          190
83 tca cgc cga ggg cgc gca cgc aaa gcg ttg cgc gcc ctt tta cat gca      862
84 Ser Arg Arg Gly Arg Ala Arg Lys Ala Leu Arg Ala Leu Leu His Ala
85          195          200          205
87 gat ttc ttc ggg ccc gaa gat ggc tcc ata cag tgc gaa agc aac      907
88 Asp Phe Phe Gly Pro Glu Asp Gly Ser Ile Gln Cys Glu Ser Asn
89 210          215          220
91 tgatggaagt ttttcaaagt gtctgacgtt gaaaacggtg agttcacaac taggggtgaat      967
93 ggtgcacgtg atgctgcaact tttacgttta ctactttgag ggaaacaatg tctgaagaac      1027
95 aatctgccgt agcaccaaaag attcatgatg tcgccatcat cggctccggt ccagctggct      1087
97 ataccgcagc agtatatgca gcccgcgctg acctcaaccc catcatgttc gagggctatg      1147
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101 gaat      1211
104 <210> SEQ ID NO: 2
105 <211> LENGTH: 224
106 <212> TYPE: PRT
107 <213> ORGANISM: Corynebacterium glutamicum
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112 1          5          10          15
115 Pro Gln Pro Ala Gly Asp Leu Met Thr Val Leu Pro Lys Asn His Asp
116          20          25          30
119 Leu Ser Asp Thr Gln Leu Val Lys Gln Phe Ile Ser Gly Asp Ser Arg
120          35          40          45
123 Ala Phe Ser Thr Ile Ile His Arg His Glu Arg His Met Met Gln Ala
124          50          55          60
127 Ala Arg Lys Tyr Gly Arg Lys Pro Glu Asp Ala Gln Asp Ile Leu Gln
128 65          70          75          80
131 Glu Ala Leu Phe Arg Ala Ser Arg Asn Met His Leu Tyr Arg Ala Glu
132          85          90          95
135 Ala Ala Leu Gly Thr Trp Leu His Lys Leu Val Leu Asn Ser Gly Phe
136          100          105          110
139 Asp Trp Ala Thr His Arg Ser Gln Val Glu Phe Pro Ile Leu Asn Glu
140          115          120          125
143 Pro Thr Ile Asp Leu Glu Lys Asp Pro Arg Leu Ala Thr Asp Pro Leu
144          130          135          140
147 Gly Tyr Leu Asp Val Ala Met Thr Ile Arg Ser Ala Ile Asp Gln Leu
148 145          150          155          160
151 His Pro Asp Gln Arg Ile Ala Leu Ile Leu Val Asp Leu Gly Gly Tyr

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152           165           170           175
155 Thr Val Glu Asp Val Ala Glu Ile Glu Gly Ile Lys Val Gly Thr Val
156           180           185           190
159 Lys Ser Arg Arg Gly Arg Ala Arg Lys Ala Leu Arg Ala Leu Leu His
160           195           200           205
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168 <211> LENGTH: 28
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177 <211> LENGTH: 28
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179 <213> ORGANISM: Corynebacterium glutamicum
181 <400> SEQUENCE: 4
182 tgtctagaaa gcatgcggag gaatcaac                28

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VERIFICATION SUMMARY

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Input Set : A:\032301.216.seq.ST25.txt

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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date